PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/009,456**

DATE: 01/14/2002
TIME: 07:51:06

Input Set : **A:\USSEQLIST.TXT**
Output Set: **N:\CRF3\01142002\J009456.raw**

ENTERED

```
 4 <110> APPLICANT: BROWN, JAMES R.
 5       CHALKER, ALISON F.
 6       DU, WENSHANG
 7       KATZ, LISA K.
 8       MAZZULLA, MARIE JEAN
 9       PAYNE, DAVID J.
10       TRAINI, CHRISTOPHER M.
12 <120> TITLE OF INVENTION: Methods Using Mechanisms of Action of
13       AroA
15 <130> FILE REFERENCE: GM50053
17 <140> CURRENT APPLICATION NUMBER: US/10/009,456
18 <141> CURRENT FILING DATE: 2001-11-05
20 <150> PRIOR APPLICATION NUMBER: PCT/US00/12251
21 <151> PRIOR FILING DATE: 2000-05-04
23 <150> PRIOR APPLICATION NUMBER: 60/133,070
24 <151> PRIOR FILING DATE: 1999-05-07
26 <160> NUMBER OF SEQ ID NOS: 4
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1284
32 <212> TYPE: DNA
33 <213> ORGANISM: Streptococcus pneumonie
35 <400> SEQUENCE: 1
36 atgaaactaa aaacaaacat tcgccattta catggtatta tccgcgtccc aggtgacaag 60
37 tctatcagcc accgttccat tatctttgga agtttggctg agggtgagac caaggtttat 120
38 gatattctgc gaggtgaaga cgttctttcg accatgcagg ttttttcgtga ccttggtgtt 180
39 gaaattgagg ataaagatgg ggttattacc gttcaaggtg taggcatggc tggcttaaaa 240
40 gcgccgcaaa atgcccttaa tatgggaaat tctggcacct cgattcgcct gatttcaggt 300
41 gtccttgctg gtgcagattt cgaagtagag atgtttggag atgatagtct ttccaaacgt 360
42 cctatggacc gtgtgaccct tccactgaaa aaaatgggcg tcagcatctc agggcaaact 420
43 gaacgagact tgcctcccct tcgcttaaaa gggacgaaaa acctaagacc tattcattat 480
44 gagttgccaa ttgcctctgc ccaagtcaag tcagccttga tgtttgcagc cttacaagct 540
45 aaggggagt cagttattat cgaaaaagag tacacccgta atcatactga agatatgttg 600
46 caacaatttg gtggtcattt aagtgtggat ggtaagaaaa tcacagtcca agggccacaa 660
47 aaattgacag gacagaaggt ggtcgtacca ggagatattt ccagtgcagc cttttggtta 720
48 gtcgcaggtt tgattgctcc aaattctcgt ctagtgctgc agaatgtggg gataaacgaa 780
49 actcgcaccg gtattattga tgtcattcgt gccatgggtg gaaaattgga ataactgaa 840
50 atcgatccag tcgctaaatc tgcaaccttg attgttgagt cttctgactt gaaaggaaca 900
51 gagatttgtg gcgctttgat tccacgtttg attgatgaat tgcctattat tgccctactt 960
52 gcgacccaag cccaaggtgt aacagttatc aaggatgctg aggagctcaa ggtcaaggaa 1020
53 acagaccgta ttcaggttgt ggcagacgcc ttaaatagta tgggagcaga tattactcct 1080
54 acggcagatg ggatgattat caaaggaaaa tcagctcttc acggtgctag agtcaatacg 1140
55 tttggtgacc accgtatcgg catgatgaca gctatcgcag ccctattggt tgcagatgga 1200
56 gaggtggagc ttgaccgtgc agaagccatc aataccagct atcctagttt ctttgatgat 1260
57 ttggagagct tgattcatgg ctaa                                      1284
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 427
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61 <212> TYPE: PRT
62 <213> ORGANISM: Streptococcus pneumoniae
64 <400> SEQUENCE: 2
65 Met Lys Leu Lys Thr Asn Ile Arg His Leu His Gly Ile Ile Arg Val
66 1   5   10   15
67 Pro Gly Asp Lys Ser Ile Ser His Arg Ser Ile Ile Phe Gly Ser Leu
68   20   25   30
69 Ala Glu Gly Glu Thr Lys Val Tyr Asp Ile Leu Arg Gly Glu Asp Val
70   35   40   45
71 Leu Ser Thr Met Gln Val Phe Arg Asp Leu Gly Val Glu Ile Glu Asp
72   50   55   60
73 Lys Asp Gly Val Ile Thr Val Gln Gly Val Gly Met Ala Gly Leu Lys
74 65   70   75   80
75 Ala Pro Gln Asn Ala Leu Asn Met Gly Asn Ser Gly Thr Ser Ile Arg
76   85   90   95
77 Leu Ile Ser Gly Val Leu Ala Gly Ala Asp Phe Glu Val Glu Met Phe
78   100   105   110
79 Gly Asp Asp Ser Leu Ser Lys Arg Pro Met Asp Arg Val Thr Leu Pro
80   115   120   125
81 Leu Lys Lys Met Gly Val Ser Ile Ser Gly Gln Thr Glu Arg Asp Leu
82   130   135   140
83 Pro Pro Leu Arg Leu Lys Gly Thr Lys Asn Leu Arg Pro Ile His Tyr
84 145   150   155   160
85 Glu Leu Pro Ile Ala Ser Ala Gln Val Lys Ser Ala Leu Met Phe Ala
86   165   170   175
87 Ala Leu Gln Ala Lys Gly Glu Ser Val Ile Ile Glu Lys Glu Tyr Thr
88   180   185   190
89 Arg Asn His Thr Glu Asp Met Leu Gln Gln Phe Gly Gly His Leu Ser
90   195   200   205
91 Val Asp Gly Lys Lys Ile Thr Val Gln Gly Pro Gln Lys Leu Thr Gly
92   210   215   220
93 Gln Lys Val Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu
94 225   230   235   240
95 Val Ala Gly Leu Ile Ala Pro Asn Ser Arg Leu Val Leu Gln Asn Val
96   245   250   255
97 Gly Ile Asn Glu Thr Arg Thr Gly Ile Ile Asp Val Ile Arg Ala Met
98   260   265   270
99 Gly Gly Lys Leu Glu Ile Thr Glu Ile Asp Pro Val Ala Lys Ser Ala
100   275   280   285
101 Thr Leu Ile Val Glu Ser Ser Asp Leu Lys Gly Thr Glu Ile Cys Gly
102   290   295   300
103 Ala Leu Ile Pro Arg Leu Ile Asp Glu Leu Pro Ile Ile Ala Leu Leu
104 305   310   315   320
105 Ala Thr Gln Ala Gln Gly Val Thr Val Ile Lys Asp Ala Glu Glu Leu
106   325   330   335
107 Lys Val Lys Glu Thr Asp Arg Ile Gln Val Val Ala Asp Ala Leu Asn
108   340   345   350
109 Ser Met Gly Ala Asp Ile Thr Pro Thr Ala Asp Gly Met Ile Ile Lys
110   355   360   365

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Input Set : **A:\USSEQLIST.TXT**
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```
111 Gly Lys Ser Ala Leu His Gly Ala Arg Val Asn Thr Phe Gly Asp His
112      370                  375              380
113 Arg Ile Gly Met Met Thr Ala Ile Ala Ala Leu Leu Val Ala Asp Gly
114 385                  390              395                  400
115 Glu Val Glu Leu Asp Arg Ala Glu Ala Ile Asn Thr Ser Tyr Pro Ser
116                  405              410              415
117 Phe Phe Asp Asp Leu Glu Ser Leu Ile His Gly
118              420              425
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 1245
123 <212> TYPE: DNA
124 <213> ORGANISM: Streptococcus pneumoniae
126 <220> FEATURE:
127 <221> NAME/KEY: unsure
128 <222> LOCATION: (482)(483)(484)(485)(486)(487)(488)(489)(490)(491)
129 <222> LOCATION: (492)(493)(494)(495)(496)(497)(498)(499)
130 <223> OTHER INFORMATION: Where n can be represented by a, c, t, or g
132 <400> SEQUENCE: 3
133 agcttgatcg tcccaggtga caagtctatc agccaccgtt ccattatctt tggaagtttg 60
134 gctgagggtg agaccaaggt ttatgatatt ctgcgaggtg aacacgttct ttcgaccatg 120
135 caggtttttc gtgaccttgg tgttgaaatt gaggataaag atggggttat taccgttcaa 180
136 ggtgtaggca tggctggctt aaaagcgccg caaaatgccc ttaatatggg aaattctggc 240
137 acctcgattc gcctgatttc aggtgtcctt gctggtgcag atttcgaagt agagatgttt 300
138 ggagatgata gtctttccaa acgtcctatg gaccgtgtga cccttccact gaaaaaaatg 360
139 ggcgtcagca tctcagggca aactgaacga gacttgcctc cccttcgctt taaaagggac 420
140 gaaaaaccta agacctattc attatgagtt gccaattgcc tctgcccaag tcaagtcagc 480
141 cnnnnnnnnn nnnnnnnnnc taaggggggag tcagttatta tcgaaaaaga gtacaccgt 540
142 aatcatactg aagatatgtt gcaacaattt ggtggtcatt taagtgtgga tggtaagaaa 600
143 atcacagtcc aagggccaca aaaattgaca ggacagaagg tggtcgtacc aggagatatt 660
144 tccagtgcag ccttttggtt agtcgcaggt ttgattgctc caaattctcg tctagtgctg 720
145 cagaatgtgg ggataaacga aactcgcacc ggtattattg atgtcattcg tgccatgggt 780
146 ggaaaattgg aaataactga aatcgatcca gtcgctaaat ctgcaacctt gattgttgag 840
147 tcttctgact tgaaaggaac agagatttgt ggcgctttga ttccacgttt gattgatgaa 900
148 ttgcctatta ttgccctact tgcgacccaa gcccaaggtg taacagttat caaggatgct 960
149 gaggagctca aggtcaagga aacagaccgt attcaggttg tggcagacgc cttaaatagt 1020
150 atgggagcag atattactcc tacggcagat gggatgatta tcaaaggaaa atcagctctt 1080
151 cacggtgcta gagtcaatac gtttggtgac caccgtatcg gcatgatgac agctatcgca 1140
152 gccctattgg ttgcagatgg agaggtggag cttgaccgtg cagaagccat caataccagc 1200
153 tatcctagtt tctttgatga tttggagagc ttgattcatg gctaa 1245
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 415
157 <212> TYPE: PRT
158 <213> ORGANISM: Streptococcus pneumoniae
160 <220> FEATURE:
161 <221> NAME/KEY: unsure
162 <222> LOCATION: (149)((161)(162)(163)(164)(165)(166)(167)(168)
163 <223> OTHER INFORMATION: Where Xaa can be represented by any one of the twenty
naturally
164 <223> OTHER INFORMATION: occurring proteins
166 <400> SEQUENCE: 4
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,456

DATE: 01/14/2002
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Input Set : **A:\USSEQLIST.TXT**
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```
167 Ser Leu Ile Val Pro Gly Asp Lys Ser Ile Ser His Arg Ser Ile Ile
168  1               5                   10                  15
169 Phe Gly Ser Leu Ala Glu Gly Glu Thr Lys Val Tyr Asp Ile Leu Arg
170             20                  25                  30
171 Gly Glu His Val Leu Ser Thr Met Gln Val Phe Arg Asp Leu Gly Val
172         35                  40                  45
173 Glu Ile Glu Asp Lys Asp Gly Val Ile Thr Val Gln Gly Val Gly Met
174     50                  55                  60
175 Ala Gly Leu Lys Ala Pro Gln Asn Ala Leu Asn Met Gly Asn Ser Gly
176 65                  70                  75                  80
177 Thr Ser Ile Arg Leu Ile Ser Gly Val Leu Ala Gly Ala Asp Phe Glu
178                 85                  90                  95
179 Val Glu Met Phe Gly Asp Asp Ser Leu Ser Lys Arg Pro Met Asp Arg
180             100                 105                 110
181 Val Thr Leu Pro Leu Lys Lys Met Gly Val Ser Ile Ser Gly Gln Thr
182         115                 120                 125
183 Glu Arg Asp Leu Pro Pro Leu Arg Phe Lys Arg Asp Glu Lys Pro Lys
184     130                 135                 140
185 Thr Tyr Ser Leu Xaa Val Ala Asn Cys Leu Cys Pro Ser Gln Val Ser
186 145                 150                 155                 160
187 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Gly Glu Ser Val Ile Ile Glu
188                 165                 170                 175
189 Lys Glu Tyr Thr Arg Asn His Thr Glu Asp Met Leu Gln Gln Phe Gly
190             180                 185                 190
191 Gly His Leu Ser Val Asp Gly Lys Lys Ile Thr Val Gln Gly Pro Gln
192         195                 200                 205
193 Lys Leu Thr Gly Gln Lys Val Val Val Pro Gly Asp Ile Ser Ser Ala
194     210                 215                 220
195 Ala Phe Trp Leu Val Ala Gly Leu Ile Ala Pro Asn Ser Arg Leu Val
196 225                 230                 235                 240
197 Leu Gln Asn Val Gly Ile Asn Glu Thr Arg Thr Gly Ile Ile Asp Val
198                 245                 250                 255
199 Ile Arg Ala Met Gly Gly Lys Leu Glu Ile Thr Glu Ile Asp Pro Val
200             260                 265                 270
201 Ala Lys Ser Ala Thr Leu Ile Val Glu Ser Ser Asp Leu Lys Gly Thr
202         275                 280                 285
203 Glu Ile Cys Gly Ala Leu Ile Pro Arg Leu Ile Asp Glu Leu Pro Ile
204     290                 295                 300
205 Ile Ala Leu Leu Ala Thr Gln Ala Gln Gly Val Thr Val Ile Lys Asp
206 305                 310                 315                 320
207 Ala Glu Glu Leu Lys Val Lys Glu Thr Asp Arg Ile Gln Val Val Ala
208             325                 330                 335
209 Asp Ala Leu Asn Ser Met Gly Ala Asp Ile Thr Pro Thr Ala Asp Gly
210         340                 345                 350
211 Met Ile Ile Lys Gly Lys Ser Ala Leu His Gly Ala Arg Val Asn Thr
212     355                 360                 365
213 Phe Gly Asp His Arg Ile Gly Met Met Thr Ala Ile Ala Ala Leu Leu
214     370                 375                 380
215 Val Ala Asp Gly Glu Val Glu Leu Asp Arg Ala Glu Ala Ile Asn Thr
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,456

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Input Set : A:\USSEQLIST.TXT
Output Set: N:\CRF3\01142002\J009456.raw

```
216 385                        390                        395                        400
217 Ser Tyr Pro Ser Phe Phe Asp Asp Leu Glu Ser Leu Ile His Gly
218                            405                        410                        415
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/009,456

DATE: 01/14/2002
TIME: 07:51:08

Input Set : **A:\USSEQLIST.TXT**
Output Set: **N:\CRF3\01142002\J009456.raw**

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4